

Figure 1. Sequence of *C. pneumoniae* OMP (outer membrane protein) gene.

5 gtggcttgat tttgaaaaag gtccatggat gtgtttataa tgttcaaggt ctccctatcc 60
aaacattgaa atacttgcta gaggagttga acatcgatct atg gga cta ttc cat 115
Met Gly Leu Phe His
1 5

10 cta act ctc ttt gga ctt tta ttg tgt agt ctt ccc att tct ctt gtt 163
Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu Pro Ile Ser Leu Val
10 15 20

15 gct aaa ttc cct gag tct gta ggt cat aag atc ctt tat ata agt acg 211
Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile Leu Tyr Ile Ser Thr
25 30 35

20 caa tct aca cag cag gcc tta gca aca tat ctg gaa gct cta gat gcc 259
Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu Glu Ala Leu Asp Ala
40 45 50

25 tac ggt gat cat gac ttc ttc gtt tta aga aaa atc gga gaa gac tat 307
Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys Ile Gly Glu Asp Tyr
55 60 65

30 ctc aag caa agc atc cac tcc tca gat ccg caa act aga aaa agc acc 355
Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln Thr Arg Lys Ser Thr
70 75 80 85

35 atc att gga gca ggc ctg gcg gga tct tca gaa gcc ttg gac gtg ctc 403
Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu Ala Leu Asp Val Leu
90 95 100

40 tcc caa gct atg gaa act gca gac ccc ctg cag cag cta ctg gtt tta 451
Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln Gln Leu Leu Val Leu
105 110 115

45 tcg gca gtc tca gga cat ctt ggg aaa act tct gac gac tta ctg ttt 499
Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser Asp Asp Leu Leu Phe
120 125 130

50 aaa gct tta gca tct ccc tat cct gtc atc cgc tta gaa gcc gcc tat 547
Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg Leu Glu Ala Ala Tyr
135 140 145

55 aga ctt gct aat ttg aag aac act aaa gtc att gat cat cta cat tct 595
Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile Asp His Leu His Ser
150 155 160 165

60 ttc att cat aag ctt ccc gaa gaa atc caa tgc cta tct gcg gca ata 643
Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys Leu Ser Ala Ala Ile
170 175 180

55 ttc cta cgc ttg gag act gaa gaa tct gat gct tat att cgg gat ctc 691
Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala Tyr Ile Arg Asp Leu
185 190 195

60 tta gct gcc aag aaa agc gcg att cgg agt gcc aca gct ttg cag atc 739
Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala Thr Ala Leu Gln Ile
200 205 210

03662816-094500

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gga gaa tac caa caa aaa cgc ttt ctt ccg aca ctt agg aat ttg cta 787
Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr Leu Arg Asn Leu Leu
215 220 225

5 acg agt gcg tct cct caa gat caa gaa gct att ctt tat gct tta ggg 835
 Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile Leu Tyr Ala Leu Gly
 230 235 240 245

10 aag ctt aag gat ggt cag agc tac tac aat ata aaa aag caa ttg cag 883
 Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile Lys Lys Gln Leu Gln
 250 255 260

aag cct gat gtg gat gtc act tta gca gca gct caa gct tta att gct 931
Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala Gln Ala Leu Ile Ala

15 265 270 275

ttg ggg aaa gaa gag gac gct ctt ccc gtg ata aaa aag caa gca ctt 979
Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile Lys Lys Gln Ala Leu
280 285 290

gag gag cgg cct cga gcc ctg tat gcc tta cgg cat cta ccc tct gag 1027
Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg His Leu Pro Ser Glu
295 300 305

25 ata ggg att ccg att gcc ctg ccg ata ttc cta aaa act aag aac agc 1075
 Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu Lys Thr Lys Asn Ser
 310 315 320 325

30 gaa gcc aag ttg aat gta gct tta gct ctc tta gag tta ggg tgt gac 1123
 Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu Glu Leu Gly Cys Asp
 330 335 340

acc cct aaa cta ctg gaa tac att acc gaa agg ctt gtc caa cca cat 1171
Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg Leu Val Gln Pro His
35 345 350 355

tat	aat	gag	act	cta	gcc	ttg	agt	ttc	tct	aag	ggg	cgt	act	tta	caa	1219
Tyr	Asn	Glu	Thr	Leu	Ala	Leu	Ser	Phe	Ser	Lys	Gly	Arg	Thr	Leu	Gln	
		360					365					370				

aat tgg aag cgg gtg aac atc ata gtc cct caa gat ccc cag gag agg 1267
Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln Asp Pro Gln Glu Arg
375 380 385

45 gaa agg ttg ctc tcc aca acc cga ggt ctt gaa gag cag atc ctt acg 1315
 Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu Glu Gln Ile Leu Thr
 390 395 400 405

50 ttt ctc ttc cgc cta cct aaa gaa gct tac ctc ccc tgt att tat aag 1363
 Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu Pro Cys Ile Tyr Lys
 410 415 420

55 ctt ttg gcg agt cag aaa act cag ctt gcc act act gcg att tct ttt 1411
 Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr Thr Ala Ile Ser Phe
 425 430 435

tta	agt	cac	acc	tca	cat	cag	gaa	gcc	tta	gat	cta	ctt	ttc	caa	gct	1459
Leu	Ser	His	Thr	Ser	His	Gln	Glu	Ala	Leu	Asp	Leu	Leu	Phe	Gln	Ala	
		440					445					450				

gcg aag ctt cct gga gaa cct atc atc cgc gcc tat gca gat ctt gct 1507
Ala Lys Leu Pro Gly Glu Pro Ile Ile Arg Ala Tyr Ala Asp Leu Ala
455 460 465

[illegible]

att tat aat ctc acc aaa gat cct gaa aaa aaa cgt tct ctc cat gat 1555
Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys Arg Ser Leu His Asp
470 475 480 485

5 tat gca aaa aag cta att cag gaa acc ttg tta ttt gtg gac acg gaa 1603
Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu Phe Val Asp Thr Glu
 490 495 500

	aac	caa	aga	ccc	cat	ccc	agc	atg	ccc	tat	cta	cgt	tat	cag	gtc	acc	1651
10	Asn	Gln	Arg	Pro	His	Pro	Ser	Met	Pro	Tyr	Leu	Arg	Tyr	Gln	Val	Thr	
				505					510					515			

cca gaa agc cgt acg aag ctc atg ttg gat att cta gag aca cta gcc 1699
Pro Glu Ser Arg Thr Lys Leu Met Leu Asp Ile Leu Glu Thr Leu Ala
15 520 525 530

acc tgc aag tct tcc gaa gat atc cgt tta ttg ata caa ctg atg acg 1747
Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu Ile Gln Leu Met Thr
535 540 545

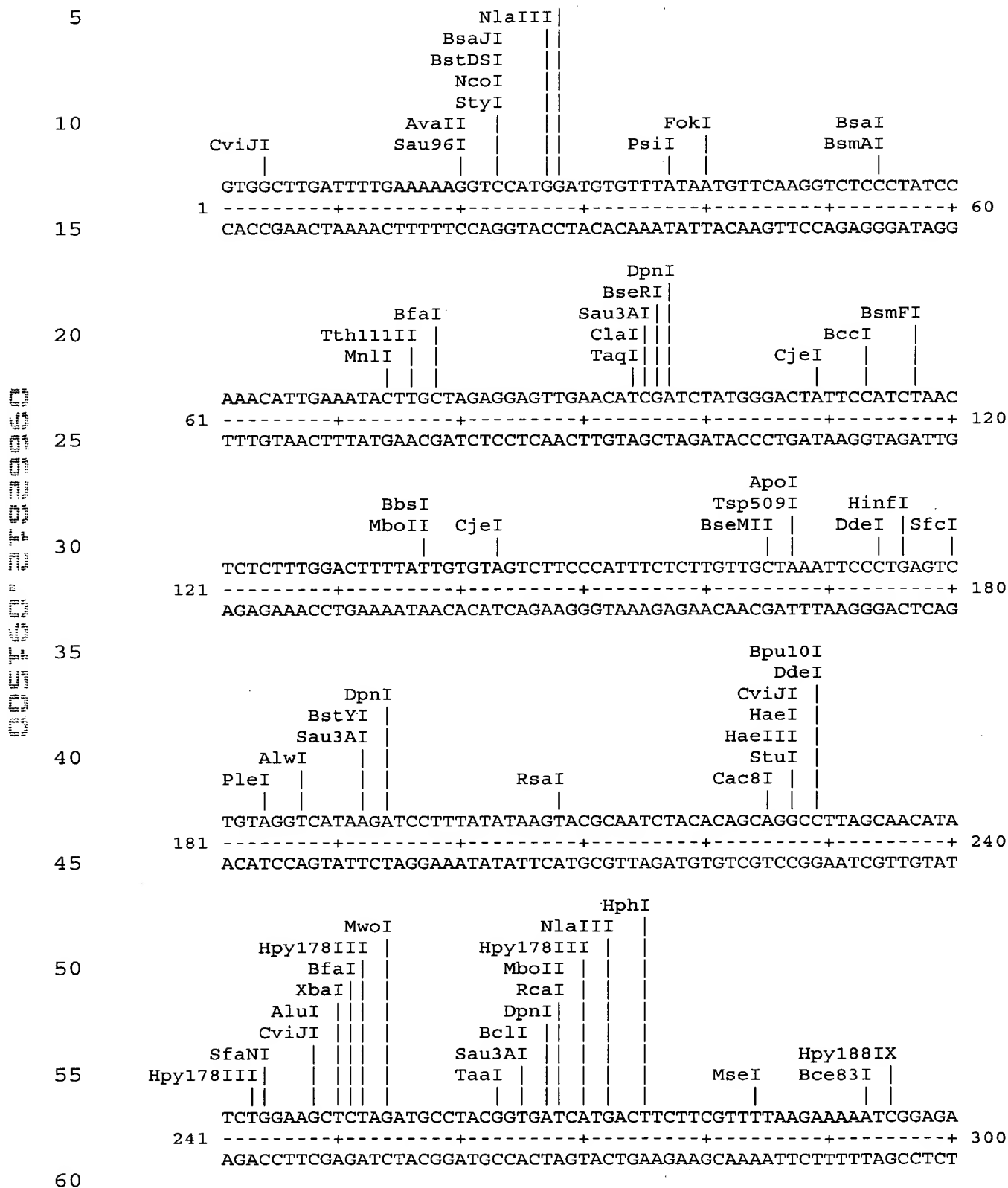
gaa gga gat gca aaa aat ttc cca gtc ctt gca ggc tta ctc ata aaa 1795
Glu Gly Asp Ala Lys Asn Phe Pro Val Leu Ala Gly Leu Leu Ile Lys
550 555 560 565

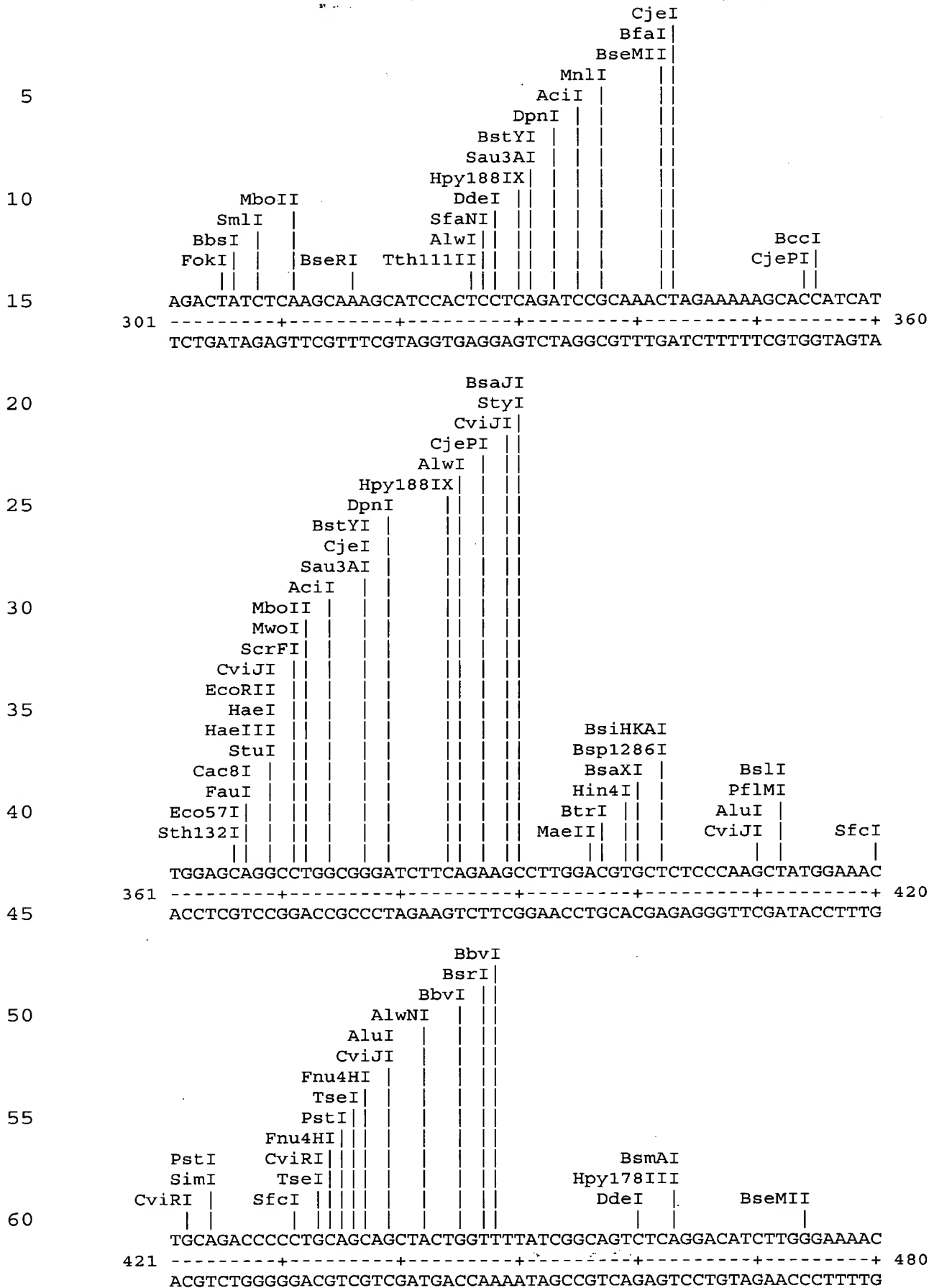
25 att gtg gag taaccccaac ctacgtctta tgaaacgttg cttcttattt 1844
Ile Val Glu

ctagcttctt ttgttcttat gggttcctca gctgatgctt tgactcatca agaggctgtg 1904

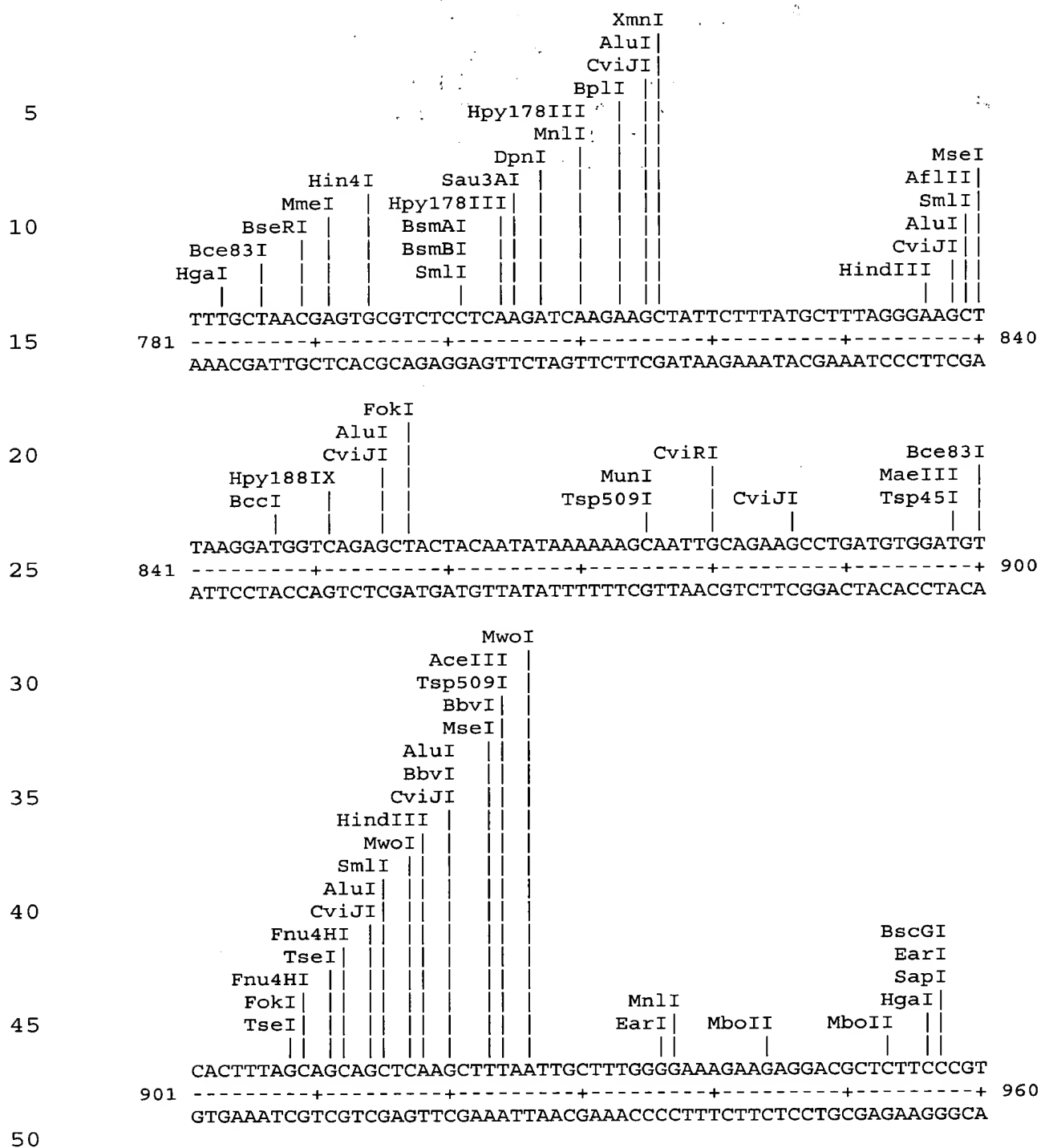
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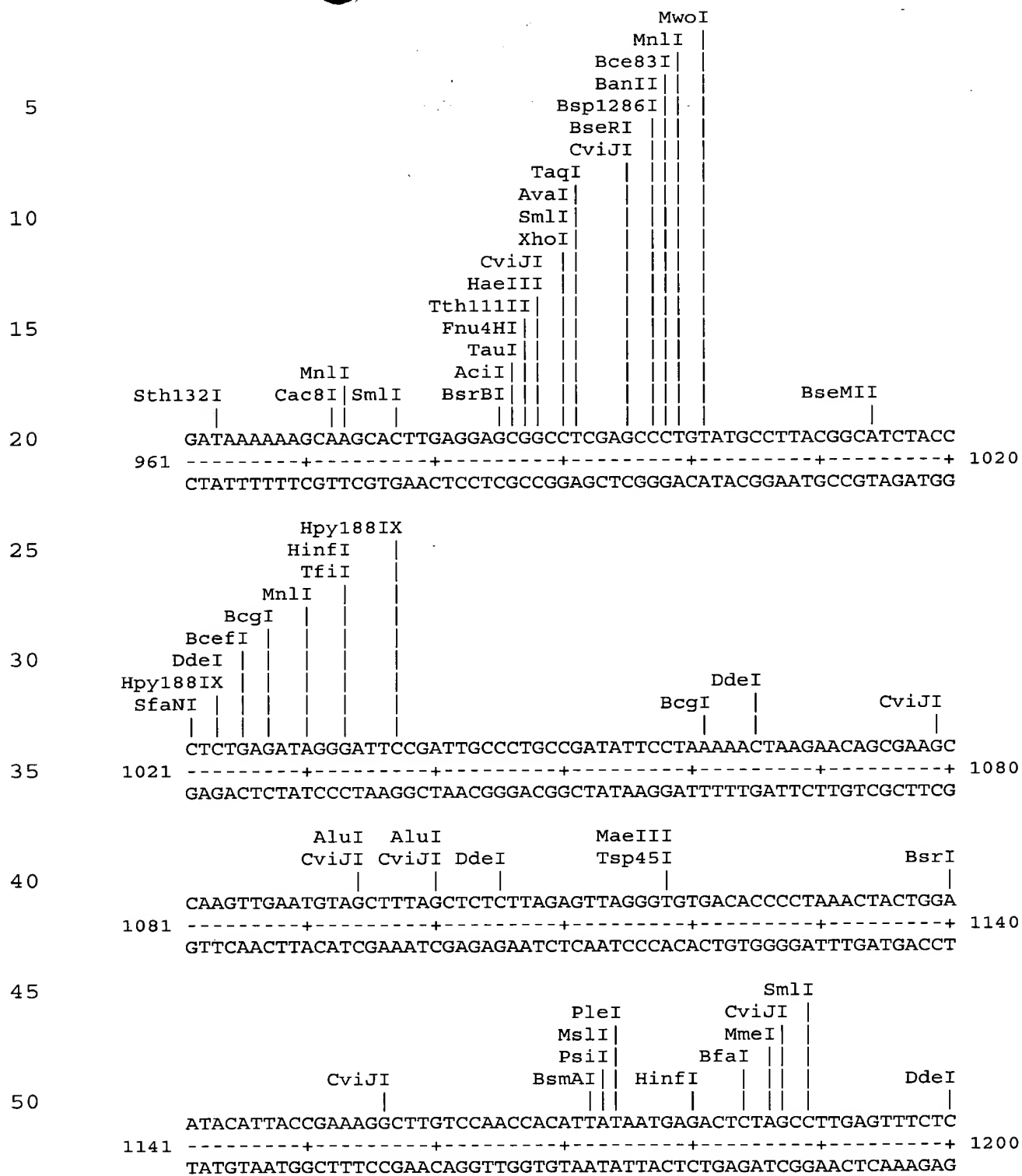
Figure 2. Restriction enzyme analysis of the *C. pneumoniae* OMP (outer membrane protein) gene.

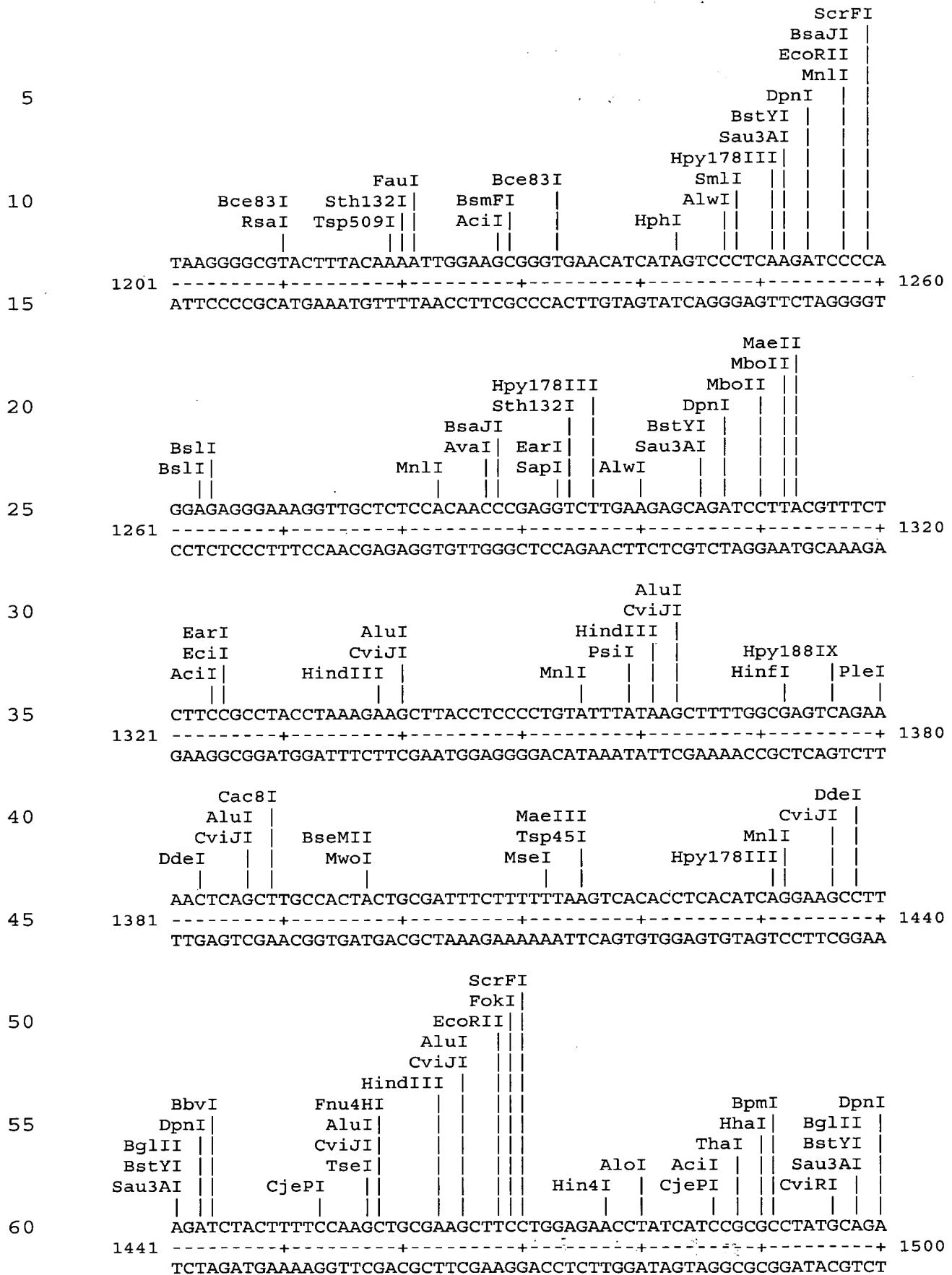


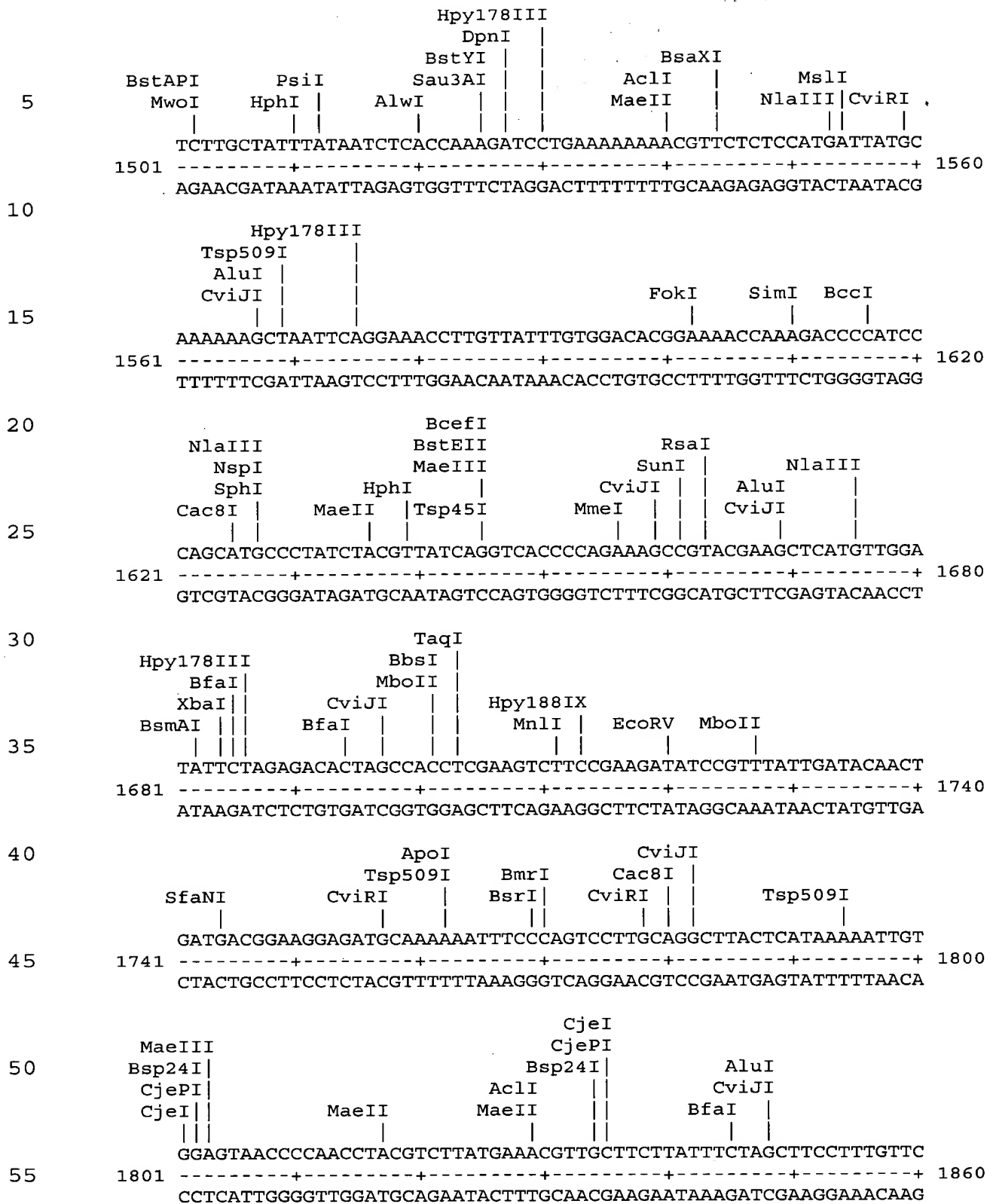


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Figure 4: Protective efficacy of DNA immunization with pCAmg002.

